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#6 OIPE

## RAW SEQUENCE LISTING

DATE: 07/09/2002

PATENT APPLICATION: US/10/066,521

TIME: 16:19:41

Input Set : A:\07334-334001.txt

Output Set: N:\CRF3\07092002\J066521.raw

ENTERED

4 <110> APPLICANT: Bertin, John  
 5 Wang, Weiye  
 6 Blatcher, Maria  
 8 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR  
 9 PROTEIN FAMILY AND USES THEREOF  
 12 <130> FILE REFERENCE: 07334-334001  
 14 <140> CURRENT APPLICATION NUMBER: 10/066,521  
 C--> 15 <141> CURRENT FILING DATE: 2002-06-25  
 17 <150> PRIOR APPLICATION NUMBER: 60/318,645  
 18 <151> PRIOR FILING DATE: 2001-09-10  
 20 <150> PRIOR APPLICATION NUMBER: 60/265,231  
 21 <151> PRIOR FILING DATE: 2001-01-31  
 23 <160> NUMBER OF SEQ ID NOS: 25  
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 1506  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Homo sapiens  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (1)...(1503)  
 36 <400> SEQUENCE: 1

37	atg gca gaa tct ttt ttt tcg gat ttt ggc ttg ttg tgg tat ctg aag	48
38	Met Ala Glu Ser Phe Phe Ser Asp Phe Gly Leu Leu Trp Tyr Leu Lys	
39	1 5 10 15	
41	gag ctc aga aag gaa gag ttt tgg aaa ttt aag gag ctc ctc aaa caa	96
42	Glu Leu Arg Lys Glu Glu Phe Trp Lys Phe Lys Glu Leu Leu Lys Gln	
43	20 25 30	
45	cct ttg gag aaa ttt gaa ctc aag cca atc ccc tgg gct gag ctg aag	144
46	Pro Leu Glu Lys Phe Glu Leu Lys Pro Ile Pro Trp Ala Glu Leu Lys	
47	35 40 45	
49	aag gcc tcc aaa gaa gat gta gca aag ctg ctg gac aaa cat tac cca	192
50	Lys Ala Ser Lys Glu Asp Val Ala Lys Leu Leu Asp Lys His Tyr Pro	
51	50 55 60	
53	gga aag cag gca tgg gag gta aca ctg aac ctg ttt cta cag atc aat	240
54	Gly Lys Gln Ala Trp Glu Val Thr Leu Asn Leu Phe Leu Gln Ile Asn	
55	65 70 75 80	
57	agg aaa gat ctc tgg aca aag gct cag gaa gag atg aga aat aag cta	288
58	Arg Lys Asp Leu Trp Thr Lys Ala Gln Glu Glu Met Arg Asn Lys Leu	
59	85 90 95	
61	aac cca tac aga aag cat atg aag gaa aca ttt caa ctc ata tgg gag	336
62	Asn Pro Tyr Arg Lys His Met Lys Glu Thr Phe Gln Leu Ile Trp Glu	
63	100 105 110	

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65	aag gaa acc tgt ctt cac gtc cct gag cat ttc tac aaa gaa acc atg	384
66	Lys Glu Thr Cys Leu His Val Pro Glu His Phe Tyr Lys Glu Thr Met	
67	115 120 125	
69	aaa aat gag tat aaa gaa ttg aat gac gca tat act gct gcg gct aga	432
70	Lys Asn Glu Tyr Lys Glu Leu Asn Asp Ala Tyr Thr Ala Ala Ala Arg	
71	130 135 140	
73	cga cac act gtg gtc ctg gaa ggt cct gat gga att gga aaa aca acc	480
74	Arg His Thr Val Val Leu Glu Gly Pro Asp Gly Ile Gly Lys Thr Thr	
75	145 150 155 160	
77	ctt tta aga aaa gtg atg ttg gac tgg gca gag gga aac tta tgg aag	528
78	Leu Leu Arg Lys Val Met Leu Asp Trp Ala Glu Gly Asn Leu Trp Lys	
79	165 170 175	
81	gac agt tac aat gag aag ctc gtc tac tgg cgg gag ctt tgc tca atg	576
82	Asp Ser Tyr Asn Glu Lys Leu Val Tyr Trp Arg Glu Leu Cys Ser Met	
83	180 185 190	
85	ttc att acc aac aag aac ttc cag att tta gac atg gaa aat acc agc	624
86	Phe Ile Thr Asn Lys Asn Phe Gln Ile Leu Asp Met Glu Asn Thr Ser	
87	195 200 205	
89	ctc gat gat ccc tcc ctg gcg att ctt tgc aaa gcg ctg gct cag cct	672
90	Leu Asp Asp Pro Ser Leu Ala Ile Leu Cys Lys Ala Leu Ala Gln Pro	
91	210 215 220	
93	gtt tgt aaa ctc cga aaa ctc ata ttt act tct gtg tac ttt gga cat	720
94	Val Cys Lys Leu Arg Lys Leu Ile Phe Thr Ser Val Tyr Phe Gly His	
95	225 230 235 240	
97	gat tca gaa tta ttt aag gca gtt ctt cac aac cct cat ctg aaa ctt	768
98	Asp Ser Glu Leu Phe Lys Ala Val Leu His Asn Pro His Leu Lys Leu	
99	245 250 255	
101	ctg agc ctg tac ggc act agc ctc tcc cag tct gac atc aga cac ctg	816
102	Leu Ser Leu Tyr Gly Thr Ser Leu Ser Gln Ser Asp Ile Arg His Leu	
103	260 265 270	
105	tgt gag acg ctg aaa cat cca atg tgc aag ata gaa gag ctg ata ctg	864
106	Cys Glu Thr Leu Lys His Pro Met Cys Lys Ile Glu Glu Leu Ile Leu	
107	275 280 285	
109	gga aag tgt gac atc tcc agt gaa gtt tgt gaa gac atc gcc tcc gtc	912
110	Gly Lys Cys Asp Ile Ser Ser Glu Val Cys Glu Asp Ile Ala Ser Val	
111	290 295 300	
113	ctg gcc tgc aac agc aag ctg aaa cac ctc tcc ttg gta gaa aat ccc	960
114	Leu Ala Cys Asn Ser Lys Leu Lys His Leu Ser Leu Val Glu Asn Pro	
115	305 310 315 320	
117	ttg agg gac gaa gga atg acg ttg ctg tgt gaa gcc ctg aag cac tca	1008
118	Leu Arg Asp Glu Gly Met Thr Leu Leu Cys Glu Ala Leu Lys His Ser	
119	325 330 335	
121	cac tgt gcc ctg gag agg ctg atg ttg atg ggc tgt ttc ctt act tcc	1056
122	His Cys Ala Leu Glu Arg Leu Met Leu Met Gly Cys Phe Leu Thr Ser	
123	340 345 350	
125	gat tcc tgt aag gac att gct gct gtt ctt att tgc aat ggg aaa ctg	1104
126	Asp Ser Cys Lys Asp Ile Ala Ala Val Leu Ile Cys Asn Gly Lys Leu	
127	355 360 365	
129	aag acc ctg aaa ctt ggg cat aat gaa ata gga gac act ggt gtc aga	1152

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130 Lys Thr Leu Lys Leu Gly His Asn Glu Ile Gly Asp Thr Gly Val Arg
131      370      375      380
133 cag tta tgt gca gct ttg cag cat cct cac tgt aaa tta gag tgt ctc      1200
134 Gln Leu Cys Ala Ala Leu Gln His Pro His Cys Lys Leu Glu Cys Leu
135 385      390      395      400
137 ggg ctg caa acg tgt ccg atc acc cgt gcc tgc tgc gac gac atc gcc      1248
138 Gly Leu Gln Thr Cys Pro Ile Thr Arg Ala Cys Cys Asp Asp Ile Ala
139      405      410      415
141 gca gca ctc atc gcc tgc aaa aca ctg agg agc ctg aac ctc gac tgg      1296
142 Ala Ala Leu Ile Ala Cys Lys Thr Leu Arg Ser Leu Asn Leu Asp Trp
143      420      425      430
145 att gcc ttg gat gct gat gca gtg gtg gtg ctg tgt gag gca ttg agc      1344
146 Ile Ala Leu Asp Ala Asp Ala Val Val Val Leu Cys Glu Ala Leu Ser
147      435      440      445
149 cac ccg gac tgt gcc ctg cag atg ctg ggg ctg cac aaa tct ggc ttt      1392
150 His Pro Asp Cys Ala Leu Gln Met Leu Gly Leu His Lys Ser Gly Phe
151      450      455      460
153 gat gaa gaa act cag aag atc ctg atg tct gtg gaa gaa aaa att ccc      1440
154 Asp Glu Glu Thr Gln Lys Ile Leu Met Ser Val Glu Glu Lys Ile Pro
155 465      470      475      480
157 cat ctg acc att tca cat gga cct tgg att gac gag gaa tac aag atc      1488
158 His Leu Thr Ile Ser His Gly Pro Trp Ile Asp Glu Glu Tyr Lys Ile
159      485      490      495
161 agg ggt gtg ctc ctc tga      1506
162 Arg Gly Val Leu Leu
163      500
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 501
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
171 <400> SEQUENCE: 2
172 Met Ala Glu Ser Phe Phe Ser Asp Phe Gly Leu Leu Trp Tyr Leu Lys
173 1      5      10      15
174 Glu Leu Arg Lys Glu Glu Phe Trp Lys Phe Lys Glu Leu Leu Lys Gln
175      20      25      30
176 Pro Leu Glu Lys Phe Glu Leu Lys Pro Ile Pro Trp Ala Glu Leu Lys
177      35      40      45
178 Lys Ala Ser Lys Glu Asp Val Ala Lys Leu Leu Asp Lys His Tyr Pro
179      50      55      60
180 Gly Lys Gln Ala Trp Glu Val Thr Leu Asn Leu Phe Leu Gln Ile Asn
181 65      70      75      80
182 Arg Lys Asp Leu Trp Thr Lys Ala Gln Glu Glu Met Arg Asn Lys Leu
183      85      90      95
184 Asn Pro Tyr Arg Lys His Met Lys Glu Thr Phe Gln Leu Ile Trp Glu
185      100      105      110
186 Lys Glu Thr Cys Leu His Val Pro Glu His Phe Tyr Lys Glu Thr Met
187      115      120      125
188 Lys Asn Glu Tyr Lys Glu Leu Asn Asp Ala Tyr Thr Ala Ala Ala Arg
189      130      135      140

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Input Set : A:\07334-334001.txt

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```

190 Arg His Thr Val Val Leu Glu Gly Pro Asp Gly Ile Gly Lys Thr Thr
191 145          150          155          160
192 Leu Leu Arg Lys Val Met Leu Asp Trp Ala Glu Gly Asn Leu Trp Lys
193          165          170          175
194 Asp Ser Tyr Asn Glu Lys Leu Val Tyr Trp Arg Glu Leu Cys Ser Met
195          180          185          190
196 Phe Ile Thr Asn Lys Asn Phe Gln Ile Leu Asp Met Glu Asn Thr Ser
197          195          200          205
198 Leu Asp Asp Pro Ser Leu Ala Ile Leu Cys Lys Ala Leu Ala Gln Pro
199          210          215          220
200 Val Cys Lys Leu Arg Lys Leu Ile Phe Thr Ser Val Tyr Phe Gly His
201 225          230          235          240
202 Asp Ser Glu Leu Phe Lys Ala Val Leu His Asn Pro His Leu Lys Leu
203          245          250          255
204 Leu Ser Leu Tyr Gly Thr Ser Leu Ser Gln Ser Asp Ile Arg His Leu
205          260          265          270
206 Cys Glu Thr Leu Lys His Pro Met Cys Lys Ile Glu Glu Leu Ile Leu
207          275          280          285
208 Gly Lys Cys Asp Ile Ser Ser Glu Val Cys Glu Asp Ile Ala Ser Val
209          290          295          300
210 Leu Ala Cys Asn Ser Lys Leu Lys His Leu Ser Leu Val Glu Asn Pro
211 305          310          315          320
212 Leu Arg Asp Glu Gly Met Thr Leu Leu Cys Glu Ala Leu Lys His Ser
213          325          330          335
214 His Cys Ala Leu Glu Arg Leu Met Leu Met Gly Cys Phe Leu Thr Ser
215          340          345          350
216 Asp Ser Cys Lys Asp Ile Ala Ala Val Leu Ile Cys Asn Gly Lys Leu
217          355          360          365
218 Lys Thr Leu Lys Leu Gly His Asn Glu Ile Gly Asp Thr Gly Val Arg
219          370          375          380
220 Gln Leu Cys Ala Ala Leu Gln His Pro His Cys Lys Leu Glu Cys Leu
221 385          390          395          400
222 Gly Leu Gln Thr Cys Pro Ile Thr Arg Ala Cys Cys Asp Asp Ile Ala
223          405          410          415
224 Ala Ala Leu Ile Ala Cys Lys Thr Leu Arg Ser Leu Asn Leu Asp Trp
225          420          425          430
226 Ile Ala Leu Asp Ala Asp Ala Val Val Leu Cys Glu Ala Leu Ser
227          435          440          445
228 His Pro Asp Cys Ala Leu Gln Met Leu Gly Leu His Lys Ser Gly Phe
229          450          455          460
230 Asp Glu Glu Thr Gln Lys Ile Leu Met Ser Val Glu Glu Lys Ile Pro
231 465          470          475          480
232 His Leu Thr Ile Ser His Gly Pro Trp Ile Asp Glu Glu Tyr Lys Ile
233          485          490          495
234 Arg Gly Val Leu Leu
235          500
237 <210> SEQ ID NO: 3
238 <211> LENGTH: 333
239 <212> TYPE: DNA

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240 <213> ORGANISM: Homo sapiens
242 <220> FEATURE:
243 <221> NAME/KEY: CDS
244 <222> LOCATION: (1)...(330)
246 <400> SEQUENCE: 3
247 atg gca gcc tct ttc ttc tct gat ttt ggt ctt atg tgg tat ctg gag      48
248 Met Ala Ala Ser Phe Phe Ser Asp Phe Gly Leu Met Trp Tyr Leu Glu
249 1 5 10 15
251 gag ctc aaa aag gag gag ttc agg aaa ttt aaa gaa cat ctc aag caa      96
252 Glu Leu Lys Lys Glu Glu Phe Arg Lys Phe Lys Glu His Leu Lys Gln
253 20 25 30
255 atg act ttg cag ctt gaa ctc aag cag att ccc tgg act gag gtc aaa      144
256 Met Thr Leu Gln Leu Glu Leu Lys Gln Ile Pro Trp Thr Glu Val Lys
257 35 40 45
259 aaa gca tcc cgg gaa gaa ctt gca aac ctc ttg atc aag cac tat gaa      192
260 Lys Ala Ser Arg Glu Glu Leu Ala Asn Leu Leu Ile Lys His Tyr Glu
261 50 55 60
263 gaa caa caa gct tgg aac ata acc tta aga atc ttt caa aag atg gat      240
264 Glu Gln Gln Ala Trp Asn Ile Thr Leu Arg Ile Phe Gln Lys Met Asp
265 65 70 75 80
267 aga aag gat ctc tgc atg aag gtc atg agg gag aga aca ggt gag gga      288
268 Arg Lys Asp Leu Cys Met Lys Val Met Arg Glu Arg Thr Gly Glu Gly
269 85 90 95
271 gtc tgg gaa ggg gga agc ctt ctt ata atg agg act atg tcc      330
272 Val Trp Glu Gly Gly Ser Leu Leu Ile Met Arg Thr Met Ser
273 100 105 110
275 taa      333
277 <210> SEQ ID NO: 4
278 <211> LENGTH: 110
279 <212> TYPE: PRT
280 <213> ORGANISM: Homo sapiens
282 <400> SEQUENCE: 4
283 Met Ala Ala Ser Phe Phe Ser Asp Phe Gly Leu Met Trp Tyr Leu Glu
284 1 5 10 15
285 Glu Leu Lys Lys Glu Glu Phe Arg Lys Phe Lys Glu His Leu Lys Gln
286 20 25 30
287 Met Thr Leu Gln Leu Glu Leu Lys Gln Ile Pro Trp Thr Glu Val Lys
288 35 40 45
289 Lys Ala Ser Arg Glu Glu Leu Ala Asn Leu Leu Ile Lys His Tyr Glu
290 50 55 60
291 Glu Gln Gln Ala Trp Asn Ile Thr Leu Arg Ile Phe Gln Lys Met Asp
292 65 70 75 80
293 Arg Lys Asp Leu Cys Met Lys Val Met Arg Glu Arg Thr Gly Glu Gly
294 85 90 95
295 Val Trp Glu Gly Gly Ser Leu Leu Ile Met Arg Thr Met Ser
296 100 105 110
298 <210> SEQ ID NO: 5
299 <211> LENGTH: 4035
300 <212> TYPE: DNA

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/066,521

DATE: 07/09/2002

TIME: 16:19:43

Input Set : A:\07334-334001.txt

Output Set: N:\CRF3\07092002\J066521.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date